

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:16:02 : Search time 172.18 Seconds
(without alignments)
221.041 Million cell updates/sec

Title: US-09-052-089a-4
Perfect score: 1075
Sequence: 1 KTIINKLFEDLAQEEENVLD.....DLQADQETITLRRKSDPP 220

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.plant:*
10: sp.podent:*
11: sp.virus:*
12: sp.vertbrate:*
13: sp.vertbrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriap:*
17: sp.archaeap:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1045	97.2	470	11 09CP4	09CP4 mus musculu
2	1045	97.2	470	11 008B54	008B54 mus musculu
3	920	85.6	469	4 09BWP2	09BWP2 homo sapien
4	906	84.3	469	4 000467	000467 homo sapien
5	740	68.8	223	11 0922M8	0922M8 mus musculu
6	522	48.6	433	13 09YGN2	09YGN2 fugu rubrip
7	180	16.7	2139	5 007369	007369 entamoeba h
8	176	16.4	2473	11 09Q284	09Q284 mus musculu
9	175.5	16.3	1827	5 020042	020042 caenorhabdi
10	175.5	16.3	1885	5 0950G9	0950G9 caenorhabdi
11	175.5	16.3	1898	5 0950H0	0950H0 caenorhabdi
12	175	16.3	324	11 09EON8	09EON8 mus musculu
13	170.5	15.9	574	4 09H810	09H810 homo sapien
14	169	15.7	397	11 099PR7	099PR7 cavia porce
15	168	15.6	484	6 028713	028713 oryctolagus
16	168	15.6	588	4 014729	014729 homo sapien

17	167	15.5	2138	5 09XZE3	09XZE3 amoeba prot
18	166	15.4	1578	10 09AV25	09AV25 oryza sativ
19	166	15.4	1958	5 096062	096062 dugesia jap
20	166	15.4	2017	5 094992	094992 drosophila
21	166	15.4	2056	5 09W0W8	09W0W8 drosophila
22	166	15.4	2057	5 094987	094987 drosophila
23	165.5	15.4	1447	11 09QYT2	09QYT2 mus musculu
24	165.5	15.4	1487	11 09QYT3	09QYT3 mus musculu
25	165.5	15.4	1871	5 09NCL3	09NCL3 drosophila
26	165	15.3	1743	5 096063	096063 dugesia jap
27	165	15.3	1941	5 026079	026079 placopecten
28	165	15.3	1950	5 026080	026080 placopecten
29	164.5	15.3	746	5 025561	025561 naegleria f
30	164.5	15.3	2501	5 09NCW7	09NCW7 drosophila
31	164	15.3	1940	5 09U7E3	09U7E3 pecten maxi
32	163	15.2	1313	10 09XIP6	09XIP6 arabidopsis
33	163	15.2	1790	3 007380	007380 saccharomyc
34	162	15.1	692	5 096720	096720 dermatophag
35	162	15.1	826	13 09YHD5	09YHD5 rana catesb
36	162	15.1	1219	5 09NJ23	09NJ23 aequipecten
37	162	15.1	1229	5 09NJ22	09NJ22 aequipecten
38	162	15.1	1243	5 09NJ21	09NJ21 aequipecten
39	162	15.1	1253	5 09NJ20	09NJ20 aequipecten
40	162	15.1	1951	5 017042	017042 aequipecten
41	161	15.0	296	4 016085	016085 homo sapien
42	160.5	14.9	1957	5 004010	004010 onchocerca
43	160.5	14.9	1963	5 002244	002244 caenorhabdi
44	160	14.9	924	5 015738	015738 dictyostell
45	160	14.9	948	4 09UIK7	09UIK7 homo sapien

ALIGNMENTS

RESULT 1
ID 09CP4 PRELIMINARY; PRT; 470 AA.
AC 09CP4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE TRAF-INTERACTING PROTEIN.
GN TRAF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; Pubmed=11217851;
RA Kawai J., Shinaigawa A., Shibata K., Yoshino M., Itoh M., Ishi Y.,
RA Arikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirral L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carinci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya K., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -i- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AK012948; BAB28567.1; -.

DR EMBL: AK012786; BAB28469.1; -
 DR MGD: MGI:1096377; Traip.
 DR InterPro: IPR001841; Znf_fing.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00184; RING; 1.
 DR ZINC-finger.
 KW ZINC-finger.
 SQ SEQUENCE 470 AA; 53149 MW; EBFABC49A9F4BF2E CRC64;

Query Match 97.2%; Score 1045; DB 11; Length 470;
 Best Local Similarity 100.0%; Pred. No. 3.6e-50;
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTIINKLFDDAOEEENVLDAEFLKNELDYSKAQLSQDKRKRDSQAIIIDTLRDTLEERN 60
 DB 56 KTIINKLFDDAOEEENVLDAEFLKNELDYSKAQLSQDKRKRDSQAIIIDTLRDTLEERN 115
 QY 61 ATVESLONALKKAMLCSTLKKQKMFLEQRDDETKQAREEHRILCKMKTMEQIELLLOS 120
 DB 116 ATVESLONALKKAMLCSTLKKQKMFLEQRDDETKQAREEHRILCKMKTMEQIELLLOS 175
 QY 121 ORSEVEEMIRDMGVGOSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKKDLVSSRSK 180
 DB 176 ORSEVEEMIRDMGVGOSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKKDLVSSRSK 235
 QY 181 LKTLNTELDQAKLELRSQKDLQASADDEITSLRK 215
 DB 236 LKTLNTELDQAKLELRSQKDLQASADDEITSLRK 270
 RESULT 2
 ID 008854 PRELIMINARY; PRT; 470 AA.
 AC 008854;
 DT 01-JUL-1997 (TREMblrel. 04, Created)
 DT 01-JUL-1997 (TREMblrel. 04, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE MTRIP.
 GN TRAIP OR MTRIP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97258620; PubMed=9104814;
 RA Lee S.Y., Lee S.Y., Choi Y.;
 RT "TRAF-interacting protein (TRIP): a novel component of the tumor
 RT necrosis factor receptor (TNFR)- and CD30-TRAF signaling complexes
 RT that inhibits TRAF2-mediated NF-kappaB activation.";
 RL J. Exp. Med. 185:1275-1285(1997).
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL: U77844; AAB52994.1; -
 DR MGD: MGI:1096377; Traip.
 DR InterPro: IPR001841; Znf_fing.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00184; RING; 1.
 DR ZINC-finger.
 KW ZINC-finger.
 SQ SEQUENCE 470 AA; 53191 MW; 00FD705B52645133 CRC64;

Query Match 97.2%; Score 1045; DB 11; Length 470;
 Best Local Similarity 100.0%; Pred. No. 3.6e-50;
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTIINKLFDDAOEEENVLDAEFLKNELDYSKAQLSQDKRKRDSQAIIIDTLRDTLEERN 60
 DB 56 KTIINKLFDDAOEEENVLDAEFLKNELDYSKAQLSQDKRKRDSQAIIIDTLRDTLEERN 115
 QY 61 ATVESLONALKKAMLCSTLKKQKMFLEQRDDETKQAREEHRILCKMKTMEQIELLLOS 120
 DB 116 ATVESLONALKKAMLCSTLKKQKMFLEQRDDETKQAREEHRILCKMKTMEQIELLLOS 175

QY 121 ORSEVEEMIRDMGVGOSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKKDLVSSRSK 180
 DB 176 ORSEVEEMIRDMGVGOSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKKDLVSSRSK 235
 QY 181 LKTLNTELDQAKLELRSQKDLQASADDEITSLRK 215
 DB 236 LKTLNTELDQAKLELRSQKDLQASADDEITSLRK 270

RESULT 3
 ID 09BWF2 PRELIMINARY; PRT; 469 AA.
 AC 09BWF2;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE TRAF INTERACTING PROTEIN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LONG CARCINOMA;
 RA Strausberg R.;
 RL Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL: BC000310; AAH00310.1; -
 DR InterPro: IPR001841; Znf_fing.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00184; RING; 1.
 DR ZINC-finger.
 KW ZINC-finger.
 SQ SEQUENCE 469 AA; 53294 MW; B9EF3808FBC5965B CRC64;

Query Match 85.6%; Score 920; DB 4; Length 469;
 Best Local Similarity 87.0%; Pred. No. 2.5e-43;
 Matches 187; Conservative 18; Mismatches 10; Indels 0; Gaps 0;

QY 1 KTIINKLFDDAOEEENVLDAEFLKNELDYSKAQLSQDKRKRDSQAIIIDTLRDTLEERN 60
 DB 56 KTIINKLFDDAOEEENVLDAEFLKNELDYVRAQLSQDKRKRDSQAIIIDTLRDTLEERN 115
 QY 61 ATVESLONALKKAMLCSTLKKQKMFLEQRDDETKQAREEHRILCKMKTMEQIELLLOS 120
 DB 116 ATVESLONALKKAMLCSTLKKQKMFLEQRDDETKQAREEHRILCKMKTMEQIELLLOS 175
 QY 121 ORSEVEEMIRDMGVGOSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKKDLVSSRSK 180
 DB 176 ORSEVEEMIRDMGVGOSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKKDLVSSRSK 235
 QY 181 LKTLNTELDQAKLELRSQKDLQASADDEITSLRK 215
 DB 236 LKTLNTELDQAKLELRSQKDLQASADDEITSLRK 270

RESULT 4
 ID 000467 PRELIMINARY; PRT; 469 AA.
 AC 000467;
 DT 01-JUL-1997 (TREMblrel. 04, Created)
 DT 01-JUL-1997 (TREMblrel. 04, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE HTRIP.
 GN HTRIP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97258620; PubMed=9104814;
 RA Lee S.Y., Lee S.Y., Choi Y.;

"TRAF-interacting protein (TRIP): a novel component of the tumor necrosis factor receptor (TNFR) - and CD30-TRAF signaling complexes that inhibits TRAF2-mediated NF-kappa activation.";
 RT J. Exp. Med. 185:1275-1285(1997).
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL: U77845; AAB52993.1; -.
 DR InterPro: IPR001841; ZnF_ring.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00184; RING; 1.
 KM zinc-finger.
 SQ SEQUENCE 469 AA; 53138 MW; 2D54ED04B84ABA4 CRC64;

Query Match 84.3%; Score 906; DB 4; Length 469;
 Best Local Similarity 86.0%; Pred. No. 1.4e-42;
 Matches 185; Conservative 18; Mismatches 12; Indels 0; Gaps 0;

QY 1 KTIINKLFFDLAQBEEVNDLAEFLKNELDVSKAQLSOKDREKRDQAIIIDTLRDTELEERN 60
 DB :|||||LFFDLAQBEEVNDLAEFLKNELDVSKAQLSOKDREKRDQAIIIDTLRDTELEERN 115
 QY 61 ATYESLONALNKAEMLCSTLKQKMFLEORODETKQAREAHRLCKMKTMEQIELLLOS 120
 DB :|||||LFFDLAQBEEVNDLAEFLKNELDVSKAQLSOKDREKRDQAIIIDTLRDTELEERN 115
 QY 116 ATYESLONALNKAEMLCSTLKQKMFLEORODETKQAREAHRLCKMKTMEQIELLLOS 175
 DB :|||||LFFDLAQBEEVNDLAEFLKNELDVSKAQLSOKDREKRDQAIIIDTLRDTELEERN 115
 QY 121 QREVEEMIRDMGVGSAVAVYCYSLKREYENLKEARKAGELADRLKDLVSSRSK 180
 DB :|||||LFFDLAQBEEVNDLAEFLKNELDVSKAQLSOKDREKRDQAIIIDTLRDTELEERN 115
 QY 176 QLEVEEMIRDMGVGSAVAVYCYSLKREYENLKEARKAGELADRLKDLVSSRSK 235
 DB :|||||LFFDLAQBEEVNDLAEFLKNELDVSKAQLSOKDREKRDQAIIIDTLRDTELEERN 115
 QY 181 LKTLNTELDQAKLELRSQAKDLSADQETSLRKK 215
 DB :|||||LFFDLAQBEEVNDLAEFLKNELDVSKAQLSOKDREKRDQAIIIDTLRDTELEERN 115
 QY 236 LQTVSELDQAKLELRSQAKDLSADQETSLRKK 270
 DB :|||||LFFDLAQBEEVNDLAEFLKNELDVSKAQLSOKDREKRDQAIIIDTLRDTELEERN 115

RESULT 5
 Q922M8 PRELIMINARY; PRT; 223 AA.
 AC Q922M8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, last annotation update)
 DE TRAF-INTERACTING PROTEIN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC006929; AAH06929.1; -.
 SQ SEQUENCE 223 AA; 25584 MW; 412291C205C43071 CRC64;

Query Match 68.8%; Score 740; DB 11; Length 223;
 Best Local Similarity 100.0%; Pred. No. 8.7e-34;
 Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTIINKLFFDLAQBEEVNDLAEFLKNELDVSKAQLSOKDREKRDQAIIIDTLRDTELEERN 60
 DB :|||||LFFDLAQBEEVNDLAEFLKNELDVSKAQLSOKDREKRDQAIIIDTLRDTELEERN 115
 QY 61 ATYESLONALNKAEMLCSTLKQKMFLEORODETKQAREAHRLCKMKTMEQIELLLOS 120
 DB :|||||LFFDLAQBEEVNDLAEFLKNELDVSKAQLSOKDREKRDQAIIIDTLRDTELEERN 115
 QY 116 ATYESLONALNKAEMLCSTLKQKMFLEORODETKQAREAHRLCKMKTMEQIELLLOS 175
 DB :|||||LFFDLAQBEEVNDLAEFLKNELDVSKAQLSOKDREKRDQAIIIDTLRDTELEERN 115
 QY 121 QREVEEMIRDMGVGSAVAVYCYSLKREYENLKEARKAGELADRLKDLVSSRSK 180
 DB :|||||LFFDLAQBEEVNDLAEFLKNELDVSKAQLSOKDREKRDQAIIIDTLRDTELEERN 115
 QY 176 QLEVEEMIRDMGVGSAVAVYCYSLKREYENLKEARKAGELADRLKDLVSSRSK 235
 DB :|||||LFFDLAQBEEVNDLAEFLKNELDVSKAQLSOKDREKRDQAIIIDTLRDTELEERN 115

RESULT 6
 Q9YGN2

ID Q9YGN2 PRELIMINARY; PRT; 433 AA.
 AC Q9YGN2;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, last annotation update)
 DE TRAF-INTERACTING PROTEIN.
 GN TRIP.
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; OC Tetraodontidae; Takifugu.
 OX NCBI_TaxID=31033;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99148833; PubMed=10025966;
 RA Coltage A.J., Clark M., Hawker K., Umranta Y., Wheller D., Bishop M., Elgar G.;
 RT "Three receptor genes for plasmalogen related growth factors in the genome of the puffer fish Fugu rubripes.";
 RL FRS Lett. 443:370-374(1999).
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL: A010317; CA09084.1; -.
 DR InterPro: IPR001841; ZnF_ring.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00184; RING; 1.
 KM zinc-finger.
 SQ SEQUENCE 433 AA; 49201 MW; A8C31AAA42168C2 CRC64;

Query Match 48.6%; Score 522; DB 13; Length 433;
 Best Local Similarity 46.0%; Pred. No. 1.4e-21;
 Matches 98; Conservative 59; Mismatches 56; Indels 0; Gaps 0;

QY 3 IINKLFFDLAQBEEVNDLAEFLKNELDVSKAQLSOKDREKRDQAIIIDTLRDTELEERNAT 62
 DB :|||||LFFDLAQBEEVNDLAEFLKNELDVSKAQLSOKDREKRDQAIIIDTLRDTELEERNAT 117
 QY 58 IISRLYEDVGLDSSVQDPESLONELDRKVNFSKREDREROKADDLMEIVELORKA 117
 DB :|||||LFFDLAQBEEVNDLAEFLKNELDVSKAQLSOKDREKRDQAIIIDTLRDTELEERNAT 62
 QY 63 VESLONALNKAEMLCSTLKQKMFLEORODETKQAREAHRLCKMKTMEQIELLLOS 122
 DB :|||||LFFDLAQBEEVNDLAEFLKNELDVSKAQLSOKDREKRDQAIIIDTLRDTELEERNAT 62
 QY 118 LENLQKVMERKELCSALRTQMTYLESQHDNTRAKAEVRLRTKMTFESLDVLOGOR 177
 DB :|||||LFFDLAQBEEVNDLAEFLKNELDVSKAQLSOKDREKRDQAIIIDTLRDTELEERNAT 62
 QY 123 SEVEEMIRDMGVGSAVAVYCYSLKREYENLKEARKAGELADRLKDLVSSRSK 182
 DB :|||||LFFDLAQBEEVNDLAEFLKNELDVSKAQLSOKDREKRDQAIIIDTLRDTELEERNAT 62
 QY 178 AEVSMITDVGIGANAEQSLTICISLKEVDNKGSLKSNENGEKRLKREVLTSNNKLN 237
 DB :|||||LFFDLAQBEEVNDLAEFLKNELDVSKAQLSOKDREKRDQAIIIDTLRDTELEERNAT 62
 QY 183 TLNTELDQAKLELRSQAKDLSADQETSLRKK 215
 DB :|||||LFFDLAQBEEVNDLAEFLKNELDVSKAQLSOKDREKRDQAIIIDTLRDTELEERNAT 62
 QY 238 KALLETRKARDKMSLQNDLTNAKEISLKK 270
 DB :|||||LFFDLAQBEEVNDLAEFLKNELDVSKAQLSOKDREKRDQAIIIDTLRDTELEERNAT 62

RESULT 7
 Q07569 PRELIMINARY; PRT; 2139 AA.
 ID Q07569
 AC Q07569; 002504;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, last annotation update)
 DE MYOSIN HEAVY CHAIN.
 GN MHCA.
 OS Entamoeba histolytica.
 OC Eukaryota; Entamoebidae; Entamoeba.
 OX NCBI_TaxID=5759;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HMI-TMS;
 RX MEDLINE=93295430; PubMed=8515774;
 RA Raymond-Denise A., Sansonetti P., Guillen N.;
 RT "Identification and characterization of a myosin heavy chain gene (mhca) from the human parasitic pathogen Entamoeba histolytica.";
 RL Mol. Biochem. Parasitol. 59:123-131(1993).
 RN [2]
 RP SEQUENCE FROM N.A.

RC STRAIN-HMI:IMSS;
RA Gullien N.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: L03534; AAB48065.1; -
DR HSP: P08799; 1MND.
DR InterPro: IPR000048; IQ.
DR InterPro: IPR01609; myosin_head.
DR Pfam: PF00612; IQ; 2.
DR Pfam: PF00063; myosin_head; 1.
DR PRINTS: PR00193; MYOSINHEAVY.
DR PRODOM: PD000355; myosin_head; 1.
DR SMART: SM00242; MISC; 1.
SQ SEQUENCE 2139 AA; 245225 MW; C68307341DB51DD1 CRC64;

Query Match 16.7%; Score 180; DB 5; Length 2139;

Best Local Similarity 27.6%; Pred. No. 0.031; Mismatches 77; Indels 28; Gaps 7;

Matches 60; Conservative 52; Mismatches 77; Indels 28; Gaps 7;
QY 11 LAQEEENVLAEPFLKNELDSVKAQLSOK-----DREKDSQAIIIDTLRPLEERNATV 63
DB 1671 VAQEEK-----QRLSDIAELKEQLEQERTTAANAEARRKIQAELEDEVKRNLEDTVNR 1726
QY 64 ESL--QNALNKAEMLCSTLKKOMKFLERODETKQAREEAHRLCKMKTMQIELLQSQ 121
DB 1727 EKLVAKNSENDAET--DSLKEEKKALE--DEIEKITDDNKLKLS-----EIDSLDRKY 1775
QY 122 RSEVEEMIRMGVGQSAVEOLAVYCVSLKKEYENLKEARKATGELADRLKKDLVSSRKL 181
DB 1776 NALDSKDSVDYKMEKFKODELKTWKDIALETEKKNHAEYTRKNG--RLKEEAEEVQVRL 1831
QY 182 KTLNTELDQAKLELRSQOKLOSADOETISLRKSSD 218
DB 1932 EALQKNLDLAQGEKAKATKQVRAADGELKSLMNELD 1868

RESULT 8
Q90284 PRELIMINARY; PRT; 2473 AA.
ID Q90284
AC Q90284;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE LEK1 (FRAGMENT).
GN 6530404A22RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99303627; PubMed=10373470;
RA Goodwin R.L., Pabon-Pena L.M., Foster G.C., Bader D.;
RT "The cloning and analysis of LEK1 identifies variations in the
RT LEK/centromere protein F/miostin gene family.";
RL J. Biol. Chem. 274:18597-18604(1999).
DR EMBL: AF194970; AAF07196.1; -
DR MGD: MGI:1915046; 6530404A22RIK.
FT NON_TER 1
SQ SEQUENCE 2473 AA; 281903 MW; 504E91A1A150A3E5 CRC64;

Query Match 16.4%; Score 176; DB 11; Length 2473;

Best Local Similarity 23.3%; Pred. No. 0.059; Mismatches 90; Indels 48; Gaps 6;

Matches 60; Conservative 60; Mismatches 90; Indels 48; Gaps 6;
QY 1 KTIINKLFFDLAQQEEN---VLDAPFLKNELDSVKAQLSOKDREKDSQAIIIDTLRDTL 56
DB 1629 KDVTETLERLEERSEENQELALIDSENKKAVERFLTKAQKDMTSLRIFELDLTVTRER 1668
QY 57 EERNAIVESIQNALNKAEMLCSTLKKOMKFLER-----ODETKQAREEA 101
DB 1689 ENLAKOQEKOSRVSELDERSLSRLLEKEKQARVOMEEDSKSAMLTQMLKELREEV 1748

QY 102 HRLCKMKTMEQIELLQSQREVEEMIRMGVGQSAVEOLAVYCVSLKKEYENLKEARK 161
DB 1749 AALCNDOETLKAQOSLIDQPEEYVHNL-----KSSIRKLVIITDADEKKNHILDLK 1801
QY 162 ATGELADRLK-----KDLV---SSRSKLTNTELDQAKLELRSQARDLQ 203
DB 1802 ESKHHADLTKDRVENLBEQELISEKNMIFQAEKSKAEIQTLSKSIQMAQVLDQLQLELI 1861
QY 204 SADOE-----ITSLKKSD 217
DB 1862 STRSENNELIKELKEDE 1879

RESULT 9

Q20042 PRELIMINARY; PRT; 1827 AA.

ID Q20042
AC Q20042;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE HYPOTHEICAL 215.1 KDA PROTEIN.
GN F35D11.11.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematozoa; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Fulton L., Wilson R.;
RT "The sequence of C. elegans cosmid F35D11.";
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RT "Direct Submission";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: U29381; AAA68757.1; -
KW Hypothetical protein.
SQ SEQUENCE 1827 AA; 215143 MW; 551C28858452A0FA CRC64;

Query Match 16.3%; Score 175.5; DB 5; Length 1827;

Best Local Similarity 25.3%; Pred. No. 0.047; Mismatches 79; Indels 31; Gaps 8;

Matches 58; Conservative 61; Mismatches 79; Indels 31; Gaps 8;

QY 5 NKLFFDLAQQEENVLD-----AEFLKNELDSVKAQLSOKDREKDSQAIIIDTLR--- 53
DB 669 NEKTDARKNDALLEVATVQOEYEQDKLEBEMNRGOEKEEADRLALDDLGNF 728
QY 54 ---DLEERNATVESIQNALNKAEMLCSTLKKOM-KFLERODETKQAREEAHRLCKM 108
DB 729 DKLNLNKKQGVTVDSLNBEI-----SSLKBDLNKSEKREKELLMELBEQKNQAE 781
QY 109 KTMQIETL-LLOSORSEVEEMIRMGVGQSAVEOLAVYCVSLKKEYENLKEARKATGELA 167
DB 782 KEEYEVALQIAEKROGVENGKCEC---EARMNELTIRIHEMLMEHDLQVYDLHTEEV 838
QY 168 DRLLKDLVSSRSKLTNTELDQAKLELRSQOKLOSADOE-ITSLKK 215
DB 839 ERLKEK---RKLEKLNBDNDGDRAEWSNERNRLESSKNEAVTELOER 884

[illegible]

RP	SEQUENCE FROM N.A.
RC	STRAIN-BRISTOL NZ;
RX	MEDLINE=99069613; PubMed=9851916;
RA	None;
RT	"Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium.";
RL	Science 282:2012-2018(1998).
RN	(2)
RP	SEQUENCE FROM N.A.
RC	STRAIN-BRISTOL NZ;
RA	Fulton L.; Wilson R.;
RL	"The sequence of C. elegans cosmid F35D11.";
RN	Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RP	SEQUENCE FROM N.A.
RC	STRAIN-BRISTOL NZ;
RA	Waterston R.;
RT	"Direct Submission.";
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR	EMBL; U29381; AAL02510.1; -.
KW	Hypothetical protein.
SQ	SEQUENCE 1898 AA; 223357 MW; 79190A6BBD60E6C CRC64;
Query Match	16.3%; Score 175.5; DB 5; Length 1898;
Best Local Similarity	25.3%; Pred. No. 0.049;
Matches 58; Conservative	61; Mismatches 79; Indels 31; Gaps 8;
OY	5 NKLFFDLAOEEENVLD-----AFPLKNELDSVKAQLSOKDREKRSOATITPTLR--- 53 :: ::: :: :: : :: : ::
Db	669 NEKYDAARKNDALLEDVATWOEKYTEQLMKLENNRRGQEKEREERADIRALLDDRGNF 728
OY	54 ----DTLEERNATVESLQNALKAKAMLCSTLKQM-KPLEQRODETQAAREAHRLCKM 108 :: :: :: : :: : :: : :: :
Db	729 DKLTNELKQKTGYTVSLNEI-----SLKEQLKSSEKKRELLRMHELEOKNEALM 781
OY	109 KTEMQIEI-LIQSORSVEEEMIRDMGVGSAYEQIALVYCSSLKKEYENLKEARKATGELA 167 :: :: :: :: :: :: :: ::
Db	782 KEELYEVKTLAEKDQGVEFNGKEC---EARNNELTKIHEMIEMEBHDQLVDHLHTEBEV 838
OY	168 DRLKRDIVSSRKLTNTLDELDAQALELRSAKDQASAGE-ITSLRKK 215 :: :: :: :: :: :: :: :: :: :
Db	839 ERLKERM--RLELEKLNQNDGDRAEWSNERNRLESSKNEAVTELQER 884
RESULT 12	
O9EQN8	PRELIMINARY; PRT; 324 AA.
ID O9EQN8 AC O9EQN8;	
DT 01-MAR-2001 (TREMBLrel. 16, Created)	
RT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)	
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)	
DE MITOSIN (FRAGMENT).	
Mus musculus (Mouse).	
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX NCBI_TaxID=10090;	
RN [1]	
RP SEQUENCE FROM N.A.	
RA Qian M., Lin D., Zhu X.;	
RT "Evolution of the internal repeat of mitotin."	
RL Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.	
DR EMBL; AF182407; AAC63426.1; -.	
DR InterPro; IPR000533; Tropomyosin.	
DR PRINTS; PR00194; TROPOMIOSIN.	
FT NON_TER 1	
FT NON_TER 324 324	
SQ SEQUENCE 324 AA; 37896 MW; A64CD5A5E1DED7D CRC64;	
Query Match	16.3%; Score 175; DB 11; Length 324;
Best Local Similarity	22.7%; Pred. No. 0.01;
Matches 57; Conservative	70; Mismatches 84; Indels 40; Gaps 8;

```

QY 1 KTIINKLFFDLAEOEEN-----VLDAEFLKNELDVSKAQLSOKDRKRDQAIIIDTLRDTL 56
D 25 KDKVENLERLEJMESENELAIIDSENKAEVETLKAQMDKMSLRFLDLVAVRSER 84
QY 57 EERNATVESLONALNKAMLCSTLKKOMKFLERODETKOAREAHN-----LKCKM 108
D 85 ENLAKOQLOKOSRVSDELCCSLR-----SLSEKQOARVOMERDSKAMLMLOTQL 137
QY 109 KTM-BOJELL-----LOSQSEVEEMIRDMGVOSANEOALVYCVSLKRE-----YENLK 157
D 138 KELVEEVAALNDQETLQAQOSLDQPEEVLHKLSSIQKLKHIDAKKKOCHILEQL 197
QY 158 EARRATGELADR-----LKKDLVSSRSKLTNTLTDQAELKLSAOKDQSAQ-----207
D 198 ESKHNHADLFKRVENLBEQELMLSEKNKHLIFQAENSAELIOTLKTETLQTMQNDQDEL 257
QY 208 EITSLRKSXD 218
D 258 ELTMTSRSEKEN 268

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RESULT 13
Q9H810 PRELIMINARY: PRT: 574 AA.
AC Q9H810;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DE 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE CDNA FLJ13161 F1S, CLONE PLACE1010896, WEAKLY SIMILAR TO NUF1
  PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
OC Mammalia: Eutheria: Primates: Catarrhini: Homiinae: Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Nagatsuna M., Hosoliri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe J., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuno Y.,
RA Ninomiya K., Iwayanagi T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK023677; BABI4636.1;
SQ SEQUENCE 574 AA; 67926 MW; 97EF904DD4EB9EAS CRC64;

```

Query Match 15.9%; Score 170.5; DB 4; Length 574;
 Best Local Similarity 22.3%; Pred. No. 0.03; Indels 63; Gaps 8;
 Matches 53; Conservative 52; Mismatches 90;

```

QY 1 KTIINKL-FFDLAEOEENVLDAEFLKNELDVSKAQLSOKDRKRDQAIIIDTLRDT 55
D 88 KTKVMKLENELEMAQSGSDTRFLRNEIQCLEQLEQKRELEDEMEKLEKKEKYNQ 147
QY 56 LEEFNATVESLONAL-----NKAEMLCSTLKKOMKFLERODE--TKOAREAHRLK 105
D 148 LALNEEAENENSKLRRENKRLKKNQOLCDDIIDYOKQIDSQKTELTSRGEQSDYRSQ 207
QY 106 CKMKTM-----BOIELLQSQSEVEEMIRDMGVOSAVQQLAVYCVSL 149
D 208 LSKNNTLQYLDLQTLTEANEKEIVQNDMRKNLEESVEM-----EKM 253
QY 150 KKEYENLEKARKATGELADRLK-----DVSSRSK-----LKTNLTELDQA 191
D 254 TDEVNRMKATVHQNDVNDIDQKKNDHNYQQLVQELTDLKSKNEEDDPINVAVAKYEW 313
QY 192 KLELRSAOKDQSAQDEITSIRKK 215

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D 314 KLISSKDEILEYQOMLNLNREK 337

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RESULT 14
Q99P7 PRELIMINARY: PRT: 397 AA.
AC Q99P7;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE ENTEROPHILIN-2L (FRAGMENT).
OC Cavia porcellus (Guinea pig).
OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
OC Mammalia: Eutheria: Rodentia: Hystriognathi: Caviidae: Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CRL (BFA) BR;
RA Gassama A., Hulin-Matsuda F., Li R.Y., Nauze M., Ragab A.,
RA Delagebeaudouf C., Simon M.F., Fauvel J., Chap H.;
RT "Enterophilins, a new family of leucine zipper proteins bearing a
  B30.2 domain and associated with enterocyte differentiation.";
RL J. Biol. Chem. 0:0-0(2001).
DR EMBL: AF126831; AAK02014.1;
DR HSP; P01100; IPOS.
DR InterPro: IPR001870; Gamma_carboxylase.
DR InterPro: IPR003345; M_repeat.
DR InterPro: IPR003877; SPRY.
DR InterPro: IPR003878; SPRY_domain.
DR Pfam: PF02370; M; 8.
DR Pfam: PF00622; SPRY; 1.
DR SMART: SM00449; SPRY; 1.
FT NON_TER 1
SQ SEQUENCE 397 AA; 48062 MW; CA78B87BA039C62 CRC64;

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Query Match 15.7%; Score 169; DB 11; Length 397;
 Best Local Similarity 25.1%; Pred. No. 0.026;
 Matches 53; Conservative 47; Mismatches 89; Indels 22; Gaps 4;

```

QY 10 DLAOEENVL-DAEFLKNELDVSKAQLSOKDRKRDQAIIIDTLRDLLEERNATVESLQ 67
D 4 DQLEKEEQLEKEKETLQTKHDQLEKGEQLEKKEKETLQTEHNDQLEKEEQLEKKEKETLQ 63
QY 68 NALNKAMLCSTLKKOMKFLERODETKOAREAHRLKCKMKTMEOLELLQSQSEVEE 127
D 64 TKHDQ-----LKEEETLQTKHDQLEKEEQLEK-----KQKETLQTKHDQLEKEEQ 110
QY 128 MIRDMGVOSAVEQLAVYCVSLKKEYENLEKARKATGELADRLKDLVSSRSKLTNTE 187
D 111 LRKDKETLQTKHDQ-----LKEEEOQLRKDKETLQTKHDQLEKEEQLEKDKETLQTK 163
QY 188 LDOAKLELRSAOKDQSAQDEITSIRKSXD 218
D 164 HDQLEKEEQLEKDKETLQTEHNDQLEKEEQID 194
RESULT 15
Q28713 PRELIMINARY: PRT: 484 AA.
AC Q28713;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE SMOOTH MUSCLE MYOSTIN HEAVY CHAIN (LIGHT MYOMYOSTIN) (FRAGMENT).
OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
OC Mammalia: Eutheria: Lagomorpha: Leporidae: Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=88124972; PubMed=3422477;
RA Nagai R., Larson D.M., Periasamy M.;

```

RT	"Characterization of a mammalian smooth muscle myosin heavy chain cDNA"		
RT	clone and its expression on various smooth muscle types."		
RL	Proc. Natl. Acad. Sci. U.S.A.	85:1047-1051	(1988).
DR	EMBL; J03614; AAA31406.1;	-.	
DR	HSSP; P13395;	2SPC.	
DR	InterPro: IPR002928;	Myosin_tail.	
DR	InterPro: IPR000533;	Tropomyosin.	
DR	Pfam: PF01576;	Myosin_tail; 1.	
DR	PRINTS: PR00194;	TROPOMYOSIN.	
FT	NON_TER	1	
SO	SEQUENCE	484 AA;	55863 MW; 07CE784AD5E9A99E CRC64;

Query Match	15.6%	Score 168;	DB 6;	Length 484;
Best Local Similarity	23.0%	Pred. No. 0.036;		
Matches 58;	Conservative 52;	Mismatches 94;	Indels 48;	Gaps 7

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OY      10 DLAQEEENVLDEFFLNEDSVKAOLOSQ-----DREKRSQAIIIDTLRPTLEE 58
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      234 DLMQJQEDDLAAERARKQADLEKEELAEELASLSGRNALQJEBKRRLERINQJLEELLEE 293
      234 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

OY      59 RNATVESIQNALNK-----AEMLCSTLKKOMKFLERODETKOAREBAHRLKCKMKTWE-- 112
      59 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      294 EOGNNEAMSDRKRKATQOAFQLSNIELATERSTAOKNESAROOLERONKBLCKSLQJEMERA 353
      294 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

OY      113 -----QTELLQSQSREVEEHIRMGQOSAEVQALVAVCSLKEVEYLKERRA 162
      113 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      354 YKSRKSTTAALEAKTAAQLEBOVEQEPARK---QAAPAKLQKRDKKLKMILLQVEDERK- 409
      354 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

OY      163 TGEIADRLKDLVSSRSKLTINTLEIDQAKLE-----LRSQKQDLOSADO-----E 208
      163 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      410 ---MAEQYKEQAENKANAKYKQLROLEEEAEESQRIINARRKQLRELDATESNEAMGRE 466
      410 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

OY      209 ITSLLKKSDDP 220
      209 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      467 VNALSKSLRGPP 478
      467 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT	16			
014729				
ID	014729	PRELIMINARY:	PRT:	588 AA.
AC	014729;			
DT	01-JAN-1998	(TREMBLrel. 05, Created)		
DT	01-JAN-1998	(TREMBLrel. 05, last sequence update)		
DE	01-DEC-2001	(TREMBLrel. 19, last annotation update)		
DE	SMOOTH MUSCLE MYOSIN HEAVY CHAIN SM2 (FRAGMENT).			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxId=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=PROSTATE;			
RA	Lin V.K., Wang D., Lee I., McConnell J.D.;			
RT	"Myosin heavy chain gene expression in normal and hyperplastic human prostate tissue."			
RL	Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF013570; AAB69326.1; -			
DR	InterPro; IPR002928; Myosin.tall.			
DR	InterPro; IPR000533; Tropomyosin.			
DR	Pfam; PF01576; Myosin.tall.1.			
DR	PRINTS; PR00194; TROPOMYOSIN.			
FT	NON_TER			
SO	SEQUENCE	588 AA:	68244 MW;	0B033C7CE10E5790 CRC64;

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Query Match Similarity      15.6%      Score 168      DB 4;      Length 588;
Best Local Similarity      24.2%      Pred No. 0.04;
Matches      61;      Conservative      52;      Mismatches      91;      Indels      48;      Gaps      9

QY      10      DLAGEENVLDAEFLKNEIDSVKQAQISOK-----DREKRSQAIIIDTPTLEE      58
Db      338      DLMQIQEDIDAAAEERRKKQADLEKEETELAEGLASSLGRNALQDEKRRLERLRIATQEELEEL      397

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OY 59 RNATVES:QONLTK-----AEMLC-----STLKQOKFLEORDEFKQAREEHNRL--- 104
Db 398 EOGNEMNSDVRRATQOAEOLSNELATENSTAKONESARQOLEEROKKELPSKIHMEGA 457
OY 105 -KCKMK-TMEDIELLOSORSEVEEMTRDMGOSAVEOLAVYCSLKEYEENLKERRKA 162
Db 458 VKSRFKSTIALLEAKINQLEBQVQBEARK---QAATKSLKQOKKKTLEILLQYEDBRK- 513
OY 163 TGEIADRLKDLVRSRSKLTTLNTELDOAKIE-----LRSQOKDLOSADO-----E 208
Db 514 --MAEQYKEQOEGKGNARVYKOLKQLEAEFEESORINANRRKLOREIDEATESNEAMGRE 570
OY 209 ITSLRKSDDP 220
Db 571 VNALSKSLRGP 582

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RESULT	17
09XZE3	
ID	09XZE3
AC	09XZE3: PRELIMINARY: PRT: 2138 AA.
DT	01-NOV-1999 (TREMBLrel. 12, Created)
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	MYOSIN HEAVY CHAIN.
OS	Amoeba proteus (Amoeba).
CC	Eukaryota; Lobosea; Gymnamoebia; Amoeblidae; Amoeba.
OX	NCBI_Textid=5775;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=D;
RX	MEDLINE=99082369; PubMed=9864850;
RA	Oh S.W., Jeon K.W.;
RT	"Characterization of myosin heavy chain and its gene in Amoeba
RL	proteus". Microbiol. 45:600-605(1998).

RP SEQUENCE FROM N.A.
RC STRAIN-D:
RA Oh S.W., Jeon K.W.:
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases
DR EMBL: AF136711; AAD33718.1; -
DR HSSP: P08799; 1MDN.
DR InterPro: IPR000048; IO.
DR InterPro: IPR001609; myosin_head.
DR InterPro: IPR004009; myosin_N.
DR Pfam: PF00612; IO; 2.
DR Pfam: PF00063; myosin_head; 1.
DR Pfam: PF02736; myosin_N; 1.
DR PRINTS: PR00193; MYOSINHEAVY.
DR ProDom: PD00355; myosin_head; 1.
DR SMART: SM00015; IO; 1.
DR SMART: SM00242; MISC; 1.
SQ SEQUENCE 218 AA; 244427 MW; D5E8BB308639FA71 CRC64

	Query Match	Similarity	15.5%	Score 167:	DB 5;	Length 2138;	
	Best Local	Similarity	25.7%:	Pred.	No.0.16:		
	Matches	Conservative	44;	Mismatches	78;	Indels	46; Gaps
OY	1	KTIINKLFEPDLAQDEBNVLDIAEFLANKNELDYSVAQAOLSQDKDRKRDQALITDLPDTLEERN	60				
Dd	1247	KLLVAKLESDDKKMKKEKYEDERDLANKLDA-----QKLSGAELDGKLNLAEEN-	1295				
OY	61	ATVESLOANLNKAEMLCSTLKQKFLEORODETQOAREBAHRLCKKM-KTMEOJELLELIQ	119				
Dd	1236	-----AKNR-----SREEKNRRDLENRLELEDOAEDGGAANSNLKKRGEGEDINLE	1342				
OY	120	SQRSEVEEMIRIMVGQGASVEOLOAYVCYLKREYEVLKARKATGEGLADRLKLDLYSSRS	179				
Dd	1343	DHQSGVDDEVODVNLSAAKKKLESELDELKLSLDNEAGRVABE-----	1388				

QY 180 KLKLTNTELDQAKLELRSAQ-----KDLSADQEIYSLKRRKSD 218
 Db 1389 KMKVYDPELHELQALASNAENKNGLVNKKVQDEVEDLNEQYEN 1434

RESULT 18

Q9AV25 PRELIMINARY; PRT; 1578 AA.
 AC 09AV25:
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE PUTATIVE KINESIN-RELATED PROTEIN.
 GN OSJNBA001014.18.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPPONBARE;
 RA Buehl C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Burr P.C.,
 RA Hsiao J., Zismann V., Pal G., Bowman C.L., Fujii C.Y., Vanaken S.E.,
 RA Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblum T.V.,
 RA Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
 RT "Oryza sativa chromosome 10 BAC OSJNBA001014 genomic sequence."
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC025783; MAK20041.1;
 DR EMBL: AC025783; MAK20041.1;
 SQ SEQUENCE 1578 AA; 178947 MW; CB7E1DB68A821A0 CRC64;

Query Match 15.4%; Score 166; DB 10; Length 1578;
 Best Local Similarity 26.1%; Pred. No. 0.14; Mismatches 87; Indels 32; Gaps 7;
 Matches 60; Conservative 51;

QY 4 INKLFDLAEEENVLDAEFLKNELDVYKAQLSQDKREK-----DSQAIIIDTLRDTL 56
 Db 777 ISKL-----EHEWVLESEF-----ISGLSOLTYLANKEKLSMLQMDRSRLITNLKDEL 826
 QY 57 EERNATVESLONALNKAKEMLCSTLKQKMFLEQRODETKQAREAHRLCKMKM-TMEIE 115
 Db 827 EQVEAQKVELKLQMDSESLITNLKDELEQVQAKVELKQMDSESLITNLKDELEQVE 886
 QY 116 L-----LQSQR--SEVEE---MIRDMVGOSAVQALAVYCVSLKREYNLKEARK 161
 Db 887 AQKVELKENQLESHRRLSEVEDESEALRSNAKIQATYDHYVEECKSLQITLADLKQKL 946
 QY 162 ATGELADRLKRDLYSSRSKLTNTLTDQAKLELRSAQKDLSADQEIYS 211
 Db 947 EVHGVAHLEQLEQSKRRTMDPCKTLESLPAKLSLQEDISLKEQSLLS 996

RESULT 19
 ID 096062 PRELIMINARY; PRT; 1958 AA.
 AC 096062:
 DT 01-MAY-1999 (TREMblrel. 10, Created)
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE MYOSIN HEAVY CHAIN.
 GN DUMHC-A.
 OS Dugesia japonica (Planarian).
 OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
 OC Paludicola; Dugesidae; Dugesia.
 OX NCBI_TaxID=6161;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kobayashi C., Kobayashi S., Orli H., Agata K., Watanabe K.;
 RT "Identification of two distinct myosin heavy chain genes."
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB015484; BAA34954.1;

DR HSSP: P24733; IMDC.
 DR InterPro: IPR001064; Crystallin.
 DR InterPro: IPR001637; GlnA_adenylin.
 DR InterPro: IPR000048; IQ.
 DR InterPro: IPR001609; myosin_head.
 DR InterPro: IPR004009; myosin_N.
 DR InterPro: IPR002928; myosin_tail.
 DR InterPro: IPR000533; tropomyosin.
 DR Pfam: PF00612; IQ; 2.
 DR Pfam: PF00063; myosin_head; 1.
 DR Pfam: PF02736; Myosin_N; 1.
 DR Pfam: PF01576; Myosin_tail; 1.
 DR PRINTS: PR00193; MYOSINHEAVY.
 DR PRINTS: PR00194; TROPOMYOSIN.
 DR Prodom: PD000355; myosin_head; 1.
 DR SMART: SM00015; IQ; 1.
 DR SMART: SM00242; Mysc; 1.
 DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
 DR PROSITE: PS00182; GlnA_ADENYLATION; UNKNOWN_1.
 DR PROSITE: PS50096; IQ; 1.
 SQ SEQUENCE 1958 AA; 224857 MW; 3FE254327DF89524 CRC64;

Query Match 15.4%; Score 166; DB 5; Length 1958;
 Best Local Similarity 21.3%; Pred. No. 0.17; Mismatches 88; Indels 24; Gaps 6;
 Matches 48; Conservative 65;

QY 5 NKLFFDLAEEENVLDAEFLKNELDVYKAQLSQDKR-----EKRSQAIIIDTLR----- 53
 Db 878 NDLFLQLOTEQDSLADAEKYSKLVQKADMESRIKLEHDLLEEDASAGLEEKKKMK 937
 QY 54 DLEERNATVESLONALNKAKEMLCSTLKQKMFLEQRODETKQAREAHRLCKMKMTMEQ 113
 Db 938 GEIEFLKRDVYDLESSLQAKQDEKTAKDQIKAL---QDIAKQDEEENKMKKKEKADE 994
 QY 114 IELLQSQRSEEMIRDMVGOSAVQALAVYCVSLKREYNLKEARKATGELADRLKRD 173
 Db 995 LQKTEESLQAEFEKVKNLNKAQAKLEQ-----TIDEMEENLSREQVRADV-EKVRK 1047
 QY 174 LVSSRSKLTNTLTDQAKLELRSAQKDLSADQEIYSLKRRKSD 218
 Db 1048 IETELKQETQTVDDIERVKREL---EQLKREKELSNASSKIED 1089

RESULT 20
 ID 094992 PRELIMINARY; PRT; 2017 AA.
 AC 094992: 024138;
 DT 01-FEB-1997 (TREMblrel. 02, Created)
 DT 01-FEB-1997 (TREMblrel. 02, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE NONMUSCLE MYOSIN-II HEAVY CHAIN.
 GN ZIP OR CG15792.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96144835; PubMed=8568878;
 RA Mansfield S.G., al-Shirawi D.Y., Ketchum A.S., Newbern E.C.,
 RA Kiehart D.P.;
 RT "Molecular organization and alternative splicing in zipper, the gene
 that encodes the Drosophila non-muscle myosin II heavy chain."
 RL J. Mol. Biol. 255:98-109(1996).
 DR EMBL: U35816; AAB09048.1;
 DR EMBL: U35816; AAB09051.1;
 DR HSSP: P10587; 1BR2.
 DR FlyBase: FBgn0005634; zip.
 DR InterPro: IPR000048; IQ.
 DR InterPro: IPR001609; myosin_head.
 DR InterPro: IPR004009; myosin_N.

DR InterPro: IPR002928; Myosin_tail.
 DR Pfam: PF00612; IQ; 1.
 DR Pfam: PF00063; Myosin_head; 1.
 DR Pfam: PF02736; Myosin_N; 1.
 DR Pfam: PF01576; Myosin_tail; 1.
 DR PRINTS: PR00193; MYOSINHEAVY.
 DR ProDom: PD000355; myosin_head; 1.
 DR SMART: SM00015; IQ; 1.
 DR SMART: SM00242; MYSC; 1.
 DR PROSITE: PSS0096; IQ; 1.
 SO SEQUENCE 2017 AA; 232089 MW; 8C76FEF2EBD02EBE CRC64;

Query Match 15.4%; Score 166; DB 5; Length 2017;
 Best Local Similarity 25.2%; Pred. No. 0.17;
 Matches 61; Conservative 47; Mismatches 96; Indels 38; Gaps 8;

QY 1 KTIINKLFFDLAEEENVDAE--FLKNELDSVKAQLSQDKREKRSQ-----AI 48
 DB 1263 KTVLEK-----AKGTLEENADLATELRVSSRQENDRRKQAESQIAELQVKLAE 1314
 QY 49 IDTLRDTLEER---NATVESIQNALNKAEMLCSTLKKQMKFLERQDDETRKQAREFAHR- 103
 DB 1315 IERRASELQEKCTKLOQEAENITNQLEAEELKASAAVKSASNMESQLTEAQQLLEETRQ 1374
 QY 104 ---LCKMKMTMEQTEILLQSORSEVEEMIRDMVGQSAVEQLAVYCVSLKKEYENLKEAR 160
 DB 1375 KLGLSSKLRQIESKEKALQQLLEEDDAKRN---ERKLAEVTTQOMKIKKAEEDADLA 1431
 QY 161 KATGELADRLKDLVSSRSKTKTL--NTELDQAKLELRSQKD---LQSADEITSRLR 213
 DB 1432 KELEEGRKRLKDIKLEALEROVKELIAQNDRIDKSKKKIQSELEDATIELEAQRKTVLE 1491
 QY 214 KK 215
 DB 1492 KK 1493

RESULT 21

Q9NMW8 PRELIMINARY; PRT; 2056 AA.
 AC Q9NMW8; 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE ZIP PROPEIN
 GN ZIP OR CG15792.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Braachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NC NCBL_TaxID=7227;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Cealniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Adayant A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Bayendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burris K.C., Busam D.A., Butler H., Cadien E., Center A., Chandra I.,
 RA Cherry J.M., Ciesley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S., Dunn P.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durkin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegyam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Matel B., McIntosh T.C., McLeod M.P., Moperson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Mostreli A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleby J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveli J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 DR EMBL: AF003465; AAF47311.1; -.
 DR HSSP: P10587; 1BR2.
 DR FlyBase: FBgn0005634; zip.
 DR InterPro: IPR000048; IQ.
 DR InterPro: IPR001609; myosin_head.
 DR InterPro: IPR004009; Myosin_N.
 DR InterPro: IPR002928; Myosin_tail.
 DR Pfam: PF00612; IQ; 1.
 DR Pfam: PF00063; myosin_head; 2.
 DR Pfam: PF02736; Myosin_N; 1.
 DR Pfam: PF01576; Myosin_tail; 1.
 DR PRINTS: PR00193; MYOSINHEAVY
 DR ProDom: PD000355; myosin_head; 1.
 DR SMART: SM00015; IQ; 1.
 DR SMART: SM00242; MYSC; 1.
 DR PROSITE: PSS0096; IQ; 1.
 SO SEQUENCE 2056 AA; 236627 MW; 1D074D9CCE1538E4 CRC64;

Query Match 15.4%; Score 166; DB 5; Length 2056;
 Best Local Similarity 25.2%; Pred. No. 0.17;
 Matches 61; Conservative 47; Mismatches 96; Indels 38; Gaps 8;

QY 1 KTIINKLFFDLAEEENVDAE--FLKNELDSVKAQLSQDKREKRSQ-----AI 48
 DB 1302 KTVLEK-----AKGTLEENADLATELRVSSRQENDRRKQAESQIAELQVKLAE 1353
 QY 49 IDTLRDTLEER---NATVESIQNALNKAEMLCSTLKKQMKFLERQDDETRKQAREFAHR- 103
 DB 1354 IERRASELQEKCTKLOQEAENITNQLEAEELKASAAVKSASNMESQLTEAQQLLEETRQ 1413
 QY 104 ---LCKMKMTMEQTEILLQSORSEVEEMIRDMVGQSAVEQLAVYCVSLKKEYENLKEAR 160
 DB 1414 KLGLSSKLRQIESKEKALQQLLEEDDAKRN---ERKLAEVTTQOMKIKKAEEDADLA 1470
 QY 161 KATGELADRLKDLVSSRSKTKTL--NTELDQAKLELRSQKD---LQSADEITSRLR 213
 DB 1471 KELEEGRKRLKDIKLEALEROVKELIAQNDRIDKSKKKIQSELEDATIELEAQRKTVLE 1530
 QY 214 KK 215
 DB 1531 KK 1532

RESULT 22

Q94987 PRELIMINARY; PRT; 2057 AA.
 AC Q94987; 01-FEB-1997 (TREMblrel. 02, Created)
 DT 01-FEB-1997 (TREMblrel. 02, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE NONMUSCLE MYOSIN-II HEAVY CHAIN.

GN ZIP OR CG15792.
OC Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96144835; PubMed=8568878;
RA Mansfield S.G., al-Shirawi D.Y., Ketchum A.S., Newbern E.C.,
RA Kiehart D.P.,
RT "Molecular organization and alternative splicing in zipper, the gene
RT that encodes the Drosophila non-muscle myosin II heavy chain."
RL J. Mol. Biol. 255:98-109(1996).
DR EMBL: U35816; AAB09049.1; -
DR EMBL: U35816; AAB09050.1; -
DR HSSP: P10587; 1BR2.
DR FLYBase; FBgn0005634; zip.
DR InterPro: IPR000048; IO.
DR InterPro: IPR001609; myosin_head.
DR InterPro: IPR004009; myosin_N.
DR InterPro: IPR002928; myosin_tail.
DR Pfam: PF00612; IO; 1.
DR Pfam: PF00063; myosin_head; 2.
DR Pfam: PF02736; Myosin_N; 1.
DR Pfam: PF01576; Myosin_tail; 1.
DR PRINTS: PR00193; MYOSINHEAVY.
DR ProDom: PD000355; myosin_head; 1.
DR SMART: SM00015; IO; 1.
DR SMART: SM00242; MYSC; 1.
DR PROSITE: PS50096; IO; 1.
SQ SEQUENCE 2057 AA; 236642 MW; 0D59519C1E83A411 CRC64;

Query Match 15.4%; Score 166; DB 5; Length 2057;
Best Local Similarity 25.2%; Pred. No. 0.17; Mismatches 96; Indels 38; Gaps 8;

Matches 61; Conservative 47; Mismatches 96; Indels 38; Gaps 8;

QY 1 KTIINKLFFDLAEEENVLDAE--FLKNELDVSKAQLSOKREKRDSQ-----AI 48
DB 1303 KTVLEK-----AKGLEENADLATELRSVSSROENRRKQASQIAELOVKLAE 1354
QY 49 IDTLRLDLEER---NATVESIQNALNKAEMLCSTLKKQMFLEDRQDETQAREAHNR- 103
DB 1355 IERARSELQEKCTKIQQAENITNQLFEALKASAAVNASMSQQLTEAQQLLSEERQ 1414
QY 104 ---LKCCKMTMEQIELLIQSRSVEEEMIRDMGVGSQAVEQLAYVCVSLKREYENLKEAR 160
DB 1415 KLGISSKLRQIESEKEALQEQLEEDDEKRRNY---ERKLAETVTQOMEIKRKAEDADLA 1471
QY 161 KATGELADRLKKDLVSSRSKLTLL---NTELDQAKLELRSQKD---LQSAODEITSLR 213
DB 1472 KELEEGKKRLKNDIEALERQVKELIAQNDRIDKSKKKIQSELEDAITLEAQRTKIVLELE 1531
QY 214 KK 215
DB 1532 KK 1533
RESULT 23
Q90YT2
ID Q90YT2 PRELIMINARY; PRT; 1447 AA.
AC Q90YT2;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-OCT-2001 (Tremblrel. 18, last sequence update)
DT 01-OCT-2001 (Tremblrel. 18, last annotation update)
DE MEA2/GOLGA3 PROTEIN.
DE MEA2/GOLGA3.
GN MEA2/GOLGA3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL6;
RA Matsukuma S.;
RT "Mea2/Golga3 Gene Product is Indispensable for Spermatogenesis in the
RT Mouse."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB029537; BAA66890.2; -
DR EMBL: AB029521; BAA66890.2; JOINED.
DR EMBL: AB029522; BAA66890.2; JOINED.
DR EMBL: AB029523; BAA66890.2; JOINED.
DR EMBL: AB029524; BAA66890.2; JOINED.
DR EMBL: AB029525; BAA66890.2; JOINED.
DR EMBL: AB029526; BAA66890.2; JOINED.
DR EMBL: AB029527; BAA66890.2; JOINED.
DR EMBL: AB029528; BAA66890.2; JOINED.
DR EMBL: AB029529; BAA66890.2; JOINED.
DR EMBL: AB029530; BAA66890.2; JOINED.
DR EMBL: AB029531; BAA66890.2; JOINED.
DR EMBL: AB029532; BAA66890.2; JOINED.
DR EMBL: AB029533; BAA66890.2; JOINED.
DR EMBL: AB029534; BAA66890.2; JOINED.
DR EMBL: AB029535; BAA66890.2; JOINED.
DR EMBL: AB029536; BAA66890.2; JOINED.
SQ SEQUENCE 1447 AA; 162776 MW; 53087BE7460B3E6F CRC64;

Query Match 15.4%; Score 165.5; DB 11; Length 1447;
Best Local Similarity 24.1%; Pred. No. 0.13; Mismatches 86; Indels 87; Gaps 12;

Matches 70; Conservative 47; Mismatches 86; Indels 87; Gaps 12;

QY 10 DLAAEEENVLDAE--FLKNE-----LDSVKAQLSOKREKR-----DSQAIDTLRD 54
DB 712 ELQREADSRDEAIHFLQKIEVLVLAQSAKSDKEELDGRARLEEDTEERISGLEQLRQ 771
QY 55 TLEERNATVESIQNALNKAEMLCSTLKKQMFLEBQ-----RODET-----KQ 96
DB 772 DLAVKSNQVNEHLODE-----TATLRKQKQVKEQVFLQKRVNVEAYRRDATSKDOLINE 824
QY 97 AREEAHRLCKCKMTMEQIELLIQSRSVE---EMIRDMGVGSQAVEQLAYVCVSLKKE 152
DB 825 LKATKRLDSEKMLROELILQGEKTVVEHSLQKQMSLVHQQMELGCHLOSVQKE 884
QY 153 YEN-----LKEA---RKATGELADRLKKDLVSSRSKLTNTLTDQ 191
DB 885 RDEMEIHQLSPDKQEQIALTEANETLTKQIEELQQAKKALTEQKKMKRLSDLSA 944
QY 192 KLELRSQKDLQSA-----DOEITSLRK-----SDP 219
DB 945 QKEMKTKHAYENAVSILSRRLQALASKAETDDELNLQRAQSTGSSDP 994
RESULT 24
Q90YT3
ID Q90YT3 PRELIMINARY; PRT; 1487 AA.
AC Q90YT3;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-OCT-2001 (Tremblrel. 18, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE MALE ENHANCED ANTIGEN 2/GOLGI AUTOANTIGEN, GOLGIN SUBFAMILY A, 3.
GN MEA2/GOLGA3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL6;
RA Matsukuma S.;
RT "Mea2/Golga3 Gene Product is Indispensable for Spermatogenesis in the
RT Mouse."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB029537; BAA66889.2; -
DR EMBL: AB029521; BAA66889.2; JOINED.


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RESULT 29
ID 025561 PRELIMINARY; PRT; 746 AA.
AC 025561;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE MYOSIN II HEAVY CHAIN (FRAGMENT).
OS Naegleria fowleri.
OC Eukaryota; Heterolobosea; Schizopyrenida; Vahlkampfiidae; Naegleria.
OX NCBI_TaxID=5763;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LEE MP;
RA Shaw D.R., Sullivan P.K., Marciano-Cabral F., Ennis H.L.;
RT "Codon usage in Naegleria fowleri."
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U04192; AAB01786.1; -.
DR InterPro; IPR002017; Spectrin.
FT NON_TER
SQ SEQUENCE 746 AA; 87781 MW; 3771A80AFC2FF43 CRC64;

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Query Match 15.3%; Score 164.5; DB 5; Length 746;
Best Local Similarity 22.7%; Pred. No. 0.083;
Matches 57; Conservative 57; Mismatches 104; Indels 33; Gaps 4;

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QY 1 KTIINKLFFDLAEEENVLDAEFLKNELDVSKAQLSOKDKREKRSQAIIPTLRDTLEERN 60
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 167 KOLONELONETNLQKSKSENERLQRELEEMKRELSLSDKQKSLDKVKSLEDKIRELT 226
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 61 ATVESLONALKAEMLCSTLKQKMFLEORODETKQA-REEAHNLKCKMKMTMEQIELLQ 119
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 227 ALLETBESSKTDLDRKSKKADKEVKRLAQQLQETQALKGCTQKKNDNRVKKLESELQ 286
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 120 SQRSSEVEIMRDVG-----VQSAYEQLAVYCVSLKKEYNLEKARKATGE 165
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 287 GVKSESRDLNLDNNTSGDMNGLKRQDESNNLVAKLKAELQKQKDLSDHGDREPEREE 346
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 166 LADLKLKDYSSRSKL-----KTLTELDQAKLELRSAOKDLQSDA---Q 207
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 347 QLDLRLKROLELTSRLSDANQKTQGEAASRONLESENRLKSEVSRLEDLQENRRLKQ 406
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 208 EITSLRKSSDD 218
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 407 EMERVQSESEV 417

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RESULT 30
ID 09NCW7 PRELIMINARY; PRT; 2501 AA.
AC 09NCW7;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE MYD PROTEIN.
GN MYD.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RL MEDLINE=20345122; Pubmed=10884435;
RA Guan Z., Pardo A., Melzig J., Nash H.A., Raabe T.;
RT "Musroom body defect, a gene involved in the control of neuroblast
RT proliferation in Drosophila, encodes a coiled-coil protein."
RL Proc. Natl. Acad. Sci. U.S.A. 97:8122-8127(2000).
DR EMBL; AF174134; AAF88146.1; -.
DR FlyBase; FBgn0002873; myd.
DR InterPro; IPR003015; HLH_Myc.
DR PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.

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FT VARIANT 6 6 W->*
SQ SEQUENCE 2501 AA; 286525 MW; F3E087071B771E62 CRC64;

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Query Match 15.3%; Score 164.5; DB 5; Length 2501;
Best Local Similarity 24.3%; Pred. No. 0.25;
Matches 66; Conservative 52; Mismatches 93; Indels 61; Gaps 11;

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QY 1 KTII-----KLFPLDAEEENVLDAEFLKNELDVSKAQLSOKD-----REK 42
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 1243 KSVIEAQTKLSDLDQREKESAQQLVDNLKVELDKERKELAQVSAFEAQTKLSDLDQRLQ 1302
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 43 RDSQAIIPTLRDTLEER-----NATVES-----LONALKAEMLCSTLK-----KOM 84
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 1303 ESAQQLVDNLKVELDKERKELAKVNSAFEAQTKLSDLDQLEKDLAQQLVPTLKVELDKER 1362
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 85 KFLQ-----RODETKQAREEHAHLKCKMT-----MEQIELLOSQRSEVE 136
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 1363 KELAQVNSPFEAQTKLSDLDQREKESAQQLVDNLKVELDKERKELAQVSAFEAQTKLSD 1422
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 127 EMTRDMGVGSNAYEQALVYCVSLKKEYNLEKARKATGELADRLKDYSSRSKLTNT 186
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 1423 DLQREKESAQQLVDNL-----MELDKERKELAQVSAIG-AQTKLSDLEQCKESVQDL- 1476
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 187 ELDOAKLELRSAOKDLQSDAEOETSLRKSSDD 218
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 1477 -VDNLKVELDKERKELAKVNSAFEAQTKLSD 1507

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RESULT 31
ID 09UTB3 PRELIMINARY; PRT; 1940 AA.
AC 09UTB3;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE MYOSIN HEAVY CHAIN.
OS Pecten maximus (King scallop) (Pilgrim's clam).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoidea;
OC Pectinoidea; Pectinidae; Pecten.
OX NCBI_TaxID=6579;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ADDUCTOR MUSCLE;
RA Jones D.P., Patel H., Chantler P.D.;
RT "Primary structure of myosin from the striated adductor muscle of the
RT Atlantic scallop, Pecten maximus."
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF134172; AAD52842.1; -.
DR HSSP; P24733; IWDG.
DR InterPro; IPR000048; IQ.
DR InterPro; IPR001609; myosin_head.
DR InterPro; IPR004009; Myosin_N.
DR InterPro; IPR002928; Myosin_tail.
DR InterPro; IPR002017; Spectrin.
DR Pfam; PF00612; IQ; 2.
DR Pfam; PF00663; myosin_head; 1.
DR Pfam; PF02736; Myosin_N; 1.
DR Pfam; PF01576; Myosin_tail; 1.
DR PRINTS; PR00193; MYOSINHEAVY.
DR ProDom; PD000355; myosin_head; 1.
DR SMART; SM00015; IQ; 1.
DR SMART; SM00242; MYSC; 1.
DR PROSITE; PS50096; IQ; 1.
SQ SEQUENCE 1940 AA; 223141 MW; A3D09DECBEB16F90 CRC64;

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Query Match 15.3%; Score 164; DB 5; Length 1940;
Best Local Similarity 24.8%; Pred. No. 0.21;
Matches 74; Conservative 49; Mismatches 89; Indels 86; Gaps 12;
QY 1 KTIINKLFFD-LAEEENVLDAEFLKNELDVSK-----AQLSOK 38
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

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RA Tsai L.-C., Chao P.-L., Ng H.-P., Chua K.-Y.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF52244; AK39511.1; -
 FT NON_TER 692 692
 SQ SEQUENCE 692 AA; 81372 MW; 61FC6380C9D7C9E2 CRC64;

Query Match 15.1%; Score 162; DB 5; Length 692;
 Best Local Similarity 24.9%; Pred. No. 0.11; Indels 54; Gaps 10;
 Matches 62; Conservative 54; Mismatches 79; Indels 54; Gaps 10;

QY 11 LAOEENLDAEFLKNEIDSVKAOISQK-----DRE-----KRDQ 46
 Db 157 LEEERRRASEN--HAHTLEVELESKQVDESEARLEELRQUTKANGDASMKSKYE 214
 QY 47 AITLTDTLEERNATV-----ESLQNALNKAEMLCSTLKQMKFLEOROD----ET 94
 Db 215 AELQAHADVEEELRRKMAOKISEVEFQLEALLNK-----CSLEKOKSRLOSEVEVLIMDL 270
 QY 95 KOAREEAHRLCKMKMTQEOITELLQSORSEVEEMIRMGVQSAVEQLAVYCVSLK--- 151
 Db 271 EKATRHAAQOLEKRVQALEKINLDKNLEVTLM-----EQAKELRVKIAELQKIQH 324
 QY 152 EYENLKEARKATGELADRLKKDLVSSRSKLTNTLEIDQAKLE---LRSQKDIQSDOE 208
 Db 325 EYEKLROQROQLARENKKITDDLAFAKSQUNDARHRIHQEIEIKRLNENDELAAKYE 384
 QY 209 ITSRLKSSD 217
 Db 385 AETLRKQEE 393

RESULT 35
 QY9YHDS PRELIMINARY; PRT; 826 AA.
 ID QY9YHDS
 AC QY9YHDS;
 DT 01-MAY-1999 (TREMblrel. 10, Created)
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE MYOSIN HEAVY CHAIN (FRAGMENT).
 GN MHC-4.
 OS Rana catesbeiana (Bull frog).
 OC Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TAIL MUSCLE; HINDIII MUSCLE;
 RA Hu H., Merrifield P., Atkinson B.G.;
 RT "Expression of the Myosin Heavy Chain Genes in the Tail Muscle of
 RT Thyroid Hormone-induced Metamorphosing Rana catesbeiana Tadpoles";
 RL Dev. Genet. 0:0-0(1999).
 DR EMBL: AF097907; AAD13772.1; -
 DR InterPro: IPR002928; Myosin_tail.
 DR InterPro: IPR000533; Tropomyosin.
 DR Pfam: PF01576; Myosin_tail; 1.
 DR PRINTS: PR00194; TROPOMYOSIN.
 FT NON_TER 1
 FT SEQUENCE 826 AA; 95362 MW; 8F9E3B0579D0F483 CRC64;

Query Match 15.1%; Score 162; DB 13; Length 826;
 Best Local Similarity 23.4%; Pred. No. 0.12; Indels 94; Gaps 12;
 Matches 66; Conservative 49; Mismatches 79; Indels 94; Gaps 12;
 QY 11 LAOEENLDAEFLKNEIDS--VKAQISQKRE---KRDQAITDTLTLE---ERNA 61
 Db 442 LEHEEARILRVQLNLNKKSEVDKRIAEKDEENQKRNQRAIDTQSTLDSLEIRSD 501
 QY 62 TV---ESLQNALNKAEMLCS-----TLKKQ 83
 Db 502 ALRLKKMGEDLNELEIQLSHANRQASEAKQLRNVOGQLKDAQLHLDDALRGQEDLKEQ 561

QY 84 MKFLEQR-----QDETQKAREAHRLCKMKMTQEOITELLQSOR----- 122
 Db 562 VAVIERRNNDQAEIERSRSLTEPTEERSKIALDE-ELIDASERQLHSONTILNSKK 620
 QY 123 -----SEVEEMIRDM---GVQSAVEQLAVYCVSLKREYENLKEARKATGELADR 169
 Db 621 LESDIAQLTNEVESVQESRNAEDKAKKAITDALMAELKEKQD-----TSAHLR 672
 QY 170 LKRLVSSRSKLTNTLELQDA-KLELRSAQKDIQSDQETITSRLKSSD 218
 Db 673 MKKNLEOS---VKDLQHRLEDAEQLAMKGGKQLOKLEVRLESELDN 719

RESULT 36
 QY9NJ23 PRELIMINARY; PRT; 1219 AA.
 ID QY9NJ23
 AC QY9NJ23;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE MYOSIN HEAVY CHAIN STRIATED MUSCLE SPECIFIC ISOFORM (FRAGMENT).
 GN MHC.
 OS Aequipecten irradians (Bay scallop).
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoida;
 OC Pectinoidae; Pectinidae; Argopecten.
 OX NCBI_TaxID=31199;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20090924; pubmed=10623517;
 RA Yamada A., Yoshio M., OIwa K., Nyitray L.;
 RT "Catchin, a novel protein in molluscan catch muscles, is produced by
 RT alternative splicing from the myosin heavy chain gene";
 RL J. Mol. Biol. 295:169-178(2000).
 DR EMBL: AF183909; AAF62391.1; -
 DR HSSP: P24733; IMDC.
 DR InterPro: IPR000048; IQ.
 DR InterPro: IPR001609; myosin_head.
 DR InterPro: IPR002928; Myosin_tail.
 DR InterPro: IPR002017; Spectrin.
 DR InterPro: IPR000533; Tropomyosin.
 DR Pfam: PF00612; IQ; 2.
 DR Pfam: PF00063; myosin_head; 1.
 DR Pfam: PF01576; Myosin_tail; 1.
 DR PRINTS: PR00194; TROPOMYOSIN.
 DR PRODOM: PD000355; myosin_head; 1.
 DR SMART: SM00015; IQ; 1.
 DR PROSITE: PS50096; IQ; 1.
 FT NON_TER 1
 FT SEQUENCE 1219 AA; 141202 MW; BAC6F574DA4AFBBB CRC64;

Query Match 15.1%; Score 162; DB 5; Length 1219;
 Best Local Similarity 24.5%; Pred. No. 0.18; Indels 86; Gaps 12;
 Matches 73; Conservative 50; Mismatches 89; Indels 86; Gaps 12;

QY 1 KTIINKLFFD-----LAOEENLDAEFLKNEIDSVKAOI-----SOK 38
 Db 185 KLIMQKADFESQIKLELERLIDDEDAADLEGIKKKMEADANLKKDIGLENTLQRAEQ 244
 QY 39 DREKRSQAITDTL-----RDTLEERN-ATVESIQ-----NALNKAE 74
 Db 245 DKAKHKNQ--ISTIQGELISQDEHIGKLNKKKALKEANKKTSLSLQAEERKCHLNK-- 300
 QY 75 MLCSTLKKQMKFLBORDETQKAREAHRLCKMK---TMEQITELLQSORSEVEEMI 129
 Db 301 -LKAKLEQALDELBNLERKKVGVDEKAKRVEQDLKSTQENVEDLERVKR-ELBENV 358
 QY 130 R-----DMGVQSAVEQLAVYCVSLKREYENLKEARKATGELADLKKDLYSSR 178
 Db 359 RRKEAEISSLSKLEDEQNLVSQLRKIKELQARIIELEELAEARNARAVEQRAELN 418
 QY 179 SKLTMTLELQDA-----KLELRSAQKDIQSA---DQETITSRLKSSD 218

Db 419 RELEELGERLDEAGAGSAQIETLNKKREAEELKIRNDEASLOHEAISALRKKHOD 476

RESULT 37

09NJ22 PRELIMINARY: PRT: 1229 AA.

AC 09NJ22: 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

DE MYOSIN HEAVY CHAIN CATCH (SMOOTH) MUSCLE SPECIFIC ISOFORM (FRAGMENT).

GN MHC.

OS Aequipecten irradians (Bay scallop).

OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoidea; Pectinidae; Argopecten.

OX NCBI_Taxid=31199;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20090924; PubMed=10623517;

RA Yamada A., Yoshio M., Owa K., Nyitray L.;

RT "Catchin, a novel protein in molluscan catch muscles, is produced by alternative splicing from the myosin heavy chain gene.";

RL J. Mol. Biol. 295:169-178(2000).

DR EMBL: AF183909; AAF62392.1; -.

DR HSSP: P24733; IMDC.

DR InterPro: IPR000048; IQ.

DR InterPro: IPR001609; myosin_head.

DR InterPro: IPR002928; myosin_tail.

DR InterPro: IPR002017; Spectrin.

DR InterPro: IPR000533; Tropomyosin.

DR Pfam: PF00063; myosin_head.1.

DR Pfam: PF01576; myosin_tail.1.

DR PRINTS: PR00194; TROPOMYOSIN.

DR PRODOM: PD000355; myosin_head.1.

DR SMART: SM00015; IQ.1.

DR PROSITE: PSS0096; IQ.1.

FT NON_TER 1

SO SEQUENCE 1229 AA; 142180 MW; 1764276CB904FDC9 CRC64;

Query Match 15.1%; Score 162; DB 5; Length 1229;

Best Local Similarity 24.5%; Pred. No. 0.18;

Matches 73; Conservative 50; Mismatches 89; Indels 86; Gaps 12;

QY 1 KTIINKLFPD-----LAQEEENVLDAEFLKNELDVKAQL-----SOK 38

Db 185 KLIMQKADFEQIKELERLDEDAADLEGIKKMEADANLKKDIGDLENTLQRAEQ 244

QY 39 DREKRDQAIIIDL-----RDTLEERN-ATVESLQ-----NALNKA 74

Db 245 DKAKHKNQ--ISTLQGEISQODEHIGKLNKKKALEANKKTSLSLAEEKCHLNK-- 300

QY 75 MLCSTLKKQKMFLEQRODETQAREEAHRLCKMK-----TMEQIELLOSQSEVEEMI 129

Db 301 -LKAKEQALDELNDLEREKVGDVEKAKRVEQDLKSTQENVEDLERVKR-ELLEENV 358

QY 130 R-----DMGVGSAVEQLAVYCVSLKKEVENLKEARKATGELADRLKDVSSR 178

Db 359 RRKAETISLSNLSKLEDEQNLVSQLRKIKELQARIIELEELAEARNARAVEQRAELN 418

QY 179 SKLKTMLTELDQA-----KLELRSQOKDLSA-----DOEITSLRKSSD 218

Db 419 RELEELGERLDEAGAGSAQIETLNKKREAEELKIRNDEASLOHEAISALRKKHOD 476

RESULT 38

09NJ21 PRELIMINARY: PRT: 1243 AA.

AC 09NJ21: 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

DE MYOSIN HEAVY CHAIN CARDIAC MUSCLE SPECIFIC ISOFORM 1 (FRAGMENT).

GN MHC.

OS Aequipecten irradians (Bay scallop).

OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoidea; Pectinidae; Argopecten.

OX NCBI_Taxid=31199;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20090924; PubMed=10623517;

RA Yamada A., Yoshio M., Owa K., Nyitray L.;

RT "Catchin, a novel protein in molluscan catch muscles, is produced by alternative splicing from the myosin heavy chain gene.";

RL J. Mol. Biol. 295:169-178(2000).

DR EMBL: AF183909; AAF62394.1; -.

DR HSSP: P24733; IMDC.

DR InterPro: IPR000048; IQ.

DR InterPro: IPR001609; myosin_head.

DR InterPro: IPR002928; myosin_tail.

DR InterPro: IPR002017; Spectrin.

DR InterPro: IPR000533; Tropomyosin.

DR Pfam: PF00063; myosin_head.1.

DR Pfam: PF01576; myosin_tail.1.

DR PRINTS: PR00194; TROPOMYOSIN.

DR PRODOM: PD000355; myosin_head.1.

DR SMART: SM00015; IQ.1.

DR PROSITE: PSS0096; IQ.1.

FT NON_TER 1

SO SEQUENCE 1243 AA; 143531 MW; B5C7219BFF2B5E8AE CRC64;

Query Match 15.1%; Score 162; DB 5; Length 1243;

Best Local Similarity 24.5%; Pred. No. 0.18;

Matches 73; Conservative 50; Mismatches 89; Indels 86; Gaps 12;

QY 1 KTIINKLFPD-----LAQEEENVLDAEFLKNELDVKAQL-----SOK 38

Db 185 KLIMQKADFEQIKELERLDEDAADLEGIKKMEADANLKKDIGDLENTLQRAEQ 244

QY 39 DREKRDQAIIIDL-----RDTLEERN-ATVESLQ-----NALNKA 74

Db 245 DKAKHKNQ--ISTLQGEISQODEHIGKLNKKKALEANKKTSLSLAEEKCHLNK-- 300

QY 75 MLCSTLKKQKMFLEQRODETQAREEAHRLCKMK-----TMEQIELLOSQSEVEEMI 129

Db 301 -LKAKEQALDELNDLEREKVGDVEKAKRVEQDLKSTQENVEDLERVKR-ELLEENV 358

QY 130 R-----DMGVGSAVEQLAVYCVSLKKEVENLKEARKATGELADRLKDVSSR 178

Db 359 RRKAETISLSNLSKLEDEQNLVSQLRKIKELQARIIELEELAEARNARAVEQRAELN 418

QY 179 SKLKTMLTELDQA-----KLELRSQOKDLSA-----DOEITSLRKSSD 218

Db 419 RELEELGERLDEAGAGSAQIETLNKKREAEELKIRNDEASLOHEAISALRKKHOD 476

RESULT 39

09NJ20 PRELIMINARY: PRT: 1253 AA.

AC 09NJ20: 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

DE MYOSIN HEAVY CHAIN CARDIAC MUSCLE SPECIFIC ISOFORM 2 (FRAGMENT).

GN MHC.

OS Aequipecten irradians (Bay scallop).

OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoidea; Pectinidae; Argopecten.

OX NCBI_Taxid=31199;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20090924; PubMed=10623517;

RA Yamada A., Yoshio M., Owa K., Nyitray L.;

RT "Catchin, a novel protein in molluscan catch muscles, is produced by


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RT alternative splicing from the myosin heavy chain gene."
RL J. Mol. Biol. 295:169-178(2000).
DR EMBL: AF183909: AAF62395.1; -.
DR HSSP: P24733; 1WDC.
DR InterPro: IPR000048; IQ.
DR InterPro: IPR001609; myosin_head.
DR InterPro: IPR002928; Myosin_tail.
DR InterPro: IPR002017; Spectrin.
DR InterPro: IPR000533; Tropomyosin.
DR Pfam: PF00063; myosin_head; 1.
DR Pfam: PF01576; myosin_tail; 1.
DR PRINTS: PR00194; TROPOMYOSIN.
DR ProDom: PD000355; myosin_head; 1.
DR SMART: SM00015; IQ; 1.
DR PROSITE: PS50096; IQ; 1.
DR NON_TER 1
FT SEQUENCE 1253 AA; 144774 MW; 56E4FF0226B58C92 CRC64;

Query Match 15.1%; Score 162; DB 5; Length 1253;
Best Local Similarity 24.5%; Pred. No. 0.18; Mismatches 89; Indels 86; Gaps 12;
Matches 73; Conservative 50;

QY 1 KTIINKLFDP-----LAQEEENVLDAEFLKNEIDSVKAOI-----SOK 38
DB 185 KLIMQKADFESEQIKELERLDEDAADLEGIKKMEADNANKDKDIGDLENTLOKAEQ 244
QY 39 DREKRDQAIIIDL-----RDILEERN-ATVESLO-----NALNKA 74
DB 245 DKAKRDNO--ISTLOGEISQODEHIGKLNKKEKALEANKKTSDSLQAEEDKCHLNK-- 300
QY 75 MLCSTLKQMKFLERODETKQAREEAHRLCKMK-----TMEQIELLLOSQSEVEEMI 129
DB 301 -LKAKLEQALDELNDNEREKKVGDEYKAKRKVEQDLKSTQENVEDLERVKR-ELEENV 358
QY 130 R-----DMVGQSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKDLVSSR 178
DB 359 RRKEAEISLSNKLDEQNLVSOQRKIKELQARIEELEELAEARNARAVEQORAEIN 418
QY 179 SKLTLNTELDQA-----KLELRSAQKDLQSA---DOEITSLRKSSD 218
DB 419 RELEELGERLDEAGATSAQIELNKKRAELIKIRDLLEASLOHEAOISALRRKHOD 476

RESULT 40
Q17042 PRELIMINARY; PRT; 1951 AA.
AC Q17042;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MYOSIN HEAVY CHAIN.
OS Aequipecten irradians (Bay scallop).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoidea;
OC Pectinoidea; Pectinidae; Argopecten.
OX NCBI_TaxID=31199;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MUSCLE, CATCH (SMOOTH) ADDUCTOR;
RX MEDLINE=95108023; PubMed=7809102;
RA Nyitrai L., Jancso A., Ochialy V., Graf L., Szent-Gyorgyi A.G.;
RT "scallop striated and smooth muscle myosin heavy-chain isoforms are
RT produced by alternative RNA splicing from a single gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:12686-12690(1994).
DR EMBL: U09782; AAC46490.1; -.
DR HSSP: P24733; 1WDC.
DR InterPro: IPR000048; IQ.
DR InterPro: IPR001609; myosin_head.
DR InterPro: IPR000409; Myosin_N.
DR InterPro: IPR002928; Myosin_tail.
DR Pfam: PF00612; IQ; 2.
DR Pfam: PF00063; myosin_head; 1.

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DR Pfam: PF02736; Myosin_N; 1.
DR Pfam: PF01576; Myosin_tail; 1.
DR PRINTS: PR00193; MYOSINHEAVY.
DR ProDom: PD000355; myosin_head; 1.
DR SMART: SM00015; IQ; 1.
DR SMART: SM00242; MYSC; 1.
DR PROSITE: PS50096; IQ; 1.
DR SEQUENCE 1951 AA; 224253 MW; 1FDC3D7D691C1410 CRC64;

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Query Match 15.1%; Score 162; DB 5; Length 1951;
Best Local Similarity 24.5%; Pred. No. 0.28;
Matches 73; Conservative 50; Mismatches 89; Indels 86; Gaps 12;

QY 1 KTIINKLFDP-----LAQEEENVLDAEFLKNEIDSVKAOI-----SOK 38
DB 907 KLIMQKADFESEQIKELERLDEDAADLEGIKKMEADNANKDKDIGDLENTLOKAEQ 966
QY 39 DREKRDQAIIIDL-----RDILEERN-ATVESLO-----NALNKA 74
DB 967 DKAKRDNO--ISTLOGEISQODEHIGKLNKKEKALEANKKTSDSLQAEEDKCHLNK-- 1022
QY 75 MLCSTLKQMKFLERODETKQAREEAHRLCKMK-----TMEQIELLLOSQSEVEEMI 129
DB 1023 -LKAKLEQALDELNDNEREKKVGDEYKAKRKVEQDLKSTQENVEDLERVKR-ELEENV 1080
QY 130 R-----DMVGQSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKDLVSSR 178
DB 1081 RRKEAEISLSNKLDEQNLVSOQRKIKELQARIEELEELAEARNARAVEQORAEIN 1140
QY 179 SKLTLNTELDQA-----KLELRSAQKDLQSA---DOEITSLRKSSD 218
DB 1141 RELEELGERLDEAGATSAQIELNKKRAELIKIRDLLEASLOHEAOISALRRKHOD 1198

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Search completed: September 4, 2002, 16:16:07
 Job time: 1491 sec
